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SEQUENCE LISTING

<110> US ONLY:
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5

OTHER COUNTRIES:
 Agriculture Victoria Services Pty Ltd AND Pig Research and Development
 Corporation AND Pfizer Products Inc.

10 <120> Novel therapeutic compositions for treating infection by *Lawsonia spp.*

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<150> AU PR1381

15 <151> 2000-11-10

<150> US 60/249596

<151> 2000-11-17

<160> 68

20 <170> PatentIn Ver. 2.0

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aaa gca ttg act act gca gca ggg atg ctg ggg ctt gct att tat tca	144
Lys Ala Leu Thr Thr Ala Ala Gly Met Leu Gly Leu Ala Ile Tyr Ser	
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ggc gta atg gga cgt cat ttt gaa aca att ttc tac tat att ttt aca	192
Gly Val Met Gly Arg His Phe Glu Thr Ile Phe Tyr Tyr Ile Phe Thr	

10010160-110901

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10 ttt att gct gtt acg gca tgg att tca tta cgt gta caa gtt ggt gca 336
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15 tta tgg act aca aag gtt ttt aaa ttt aaa tgg agt aaa ttt aat ata 384
 Leu Trp Thr Thr Lys Val Phe Lys Phe Lys Trp Ser Lys Phe Asn Ile
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20 ata aaa ggg ttg aaa gga atg ttt gct tct caa caa aca ctt gtt cga 432
 Ile Lys Gly Leu Lys Gly Met Phe Ala Ser Gln Gln Thr Leu Val Arg
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 145 150 155 160

30 atg att ata aaa gga gag ttt tca aac ttt tta cca tta tat tat gca 528
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FOOTNOTES

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<222> (1)..(786)

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att gat ggt ttt cct aat atg tta aaa gca tca ata gct ctt att cta 144
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15 act ata gtt ctt tgg ggg cgt ctt tct ctt tca gga aca caa atg cca 192
 Thr Ile Val Leu Trp Gly Arg Leu Ser Leu Ser Gly Thr Gln Met Pro
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20 gcg cat cct ttc gat cta gta ttg tta atc ata agc gag gtt ttt ctt 240
 Ala His Pro Phe Asp Leu Val Leu Leu Ile Ile Ser Glu Val Phe Leu
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ggt att gta ttg ggg ctt gcg gta aac ttt ttc ttt gca gga att caa 288
 25 Gly Ile Val Leu Gly Leu Ala Val Asn Phe Phe Phe Ala Gly Ile Gln
 85 90 95

gct ggg gga gaa att ctt gct aca caa atg ggg ttt aca atg att acg 336
 30 Ala Gly Gly Glu Ile Leu Ala Thr Gln Met Gly Phe Thr Met Ile Thr
 100 105 110

ctt gca gac cca tta act ggt aac acc aca ggt ttt att gca cat ttt 384
 Leu Ala Asp Pro Leu Thr Gly Asn Thr Thr Gly Phe Ile Ala His Phe
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Thr Ile Val Leu Trp Gly Arg Leu Ser Leu Ser Gly Thr Gln Met Pro
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 Ala His Pro Phe Asp Leu Val Leu Leu Ile Ile Ser Glu Val Phe Leu
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Gly Leu Val Val Arg Glu Ile Leu Leu Ser Glu Leu Leu Asn Met Ala
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20 Gly Met Ile Phe Val Phe Ala Leu His Val Ala Ala Pro Val Met Ser
180 185 190

Ala Leu Phe Leu Val Glu Ile Ser Leu Gly Leu Met Ala Arg Ala Ala
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25 Pro Gln Ile His Ile Met Glu Val Gly Phe Pro Val Lys Ile Gly Val
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Gly Phe Phe Phe Ile Gly Leu Leu Phe Thr Ile Leu Ser Lys Glu Thr
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gct tca gca gaa gaa gga ctt aag tgt gtt gat gta gag tct cca gat 144
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ctt gtt ttt ctt gat att tgg ctt cct ggg atg gat ggt ctt atg gct 192
Leu Val Phe Leu Asp Ile Trp Leu Pro Gly Met Asp Gly Leu Met Ala

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 65 70 75 80

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tca ggt cat gcc aca att gaa act gct gta aca gct atc cgt caa ggt 288
Ser Gly His Ala Thr Ile Glu Thr Ala Val Thr Ala Ile Arg Gln Gly

 85 90 95

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gct tat gat ttt att gaa aag cct ctt tct ttg gaa aaa gtc ctt att 336
Ala Tyr Asp Phe Ile Glu Lys Pro Leu Ser Leu Glu Lys Val Leu Ile

 100 105 110

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aca gct aat aga gct ata gaa aca gta aga tta aga agg gaa aac aaa 384
Thr Ala Asn Arg Ala Ile Glu Thr Val Arg Leu Arg Arg Glu Asn Lys

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Leu Leu Arg Thr Val Leu Pro Glu Glu Ser Glu Phe Ile Gly Gln Ser

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cct gtt atc tta aaa ttt aaa agt tta tta tca cag gtc gct cca aca 480
Pro Val Ile Leu Lys Phe Lys Ser Leu Leu Ser Gln Val Ala Pro Thr

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gat gct tgg gta cta ctt aca gga gag aat ggt aca ggt aaa gag tta 528
Asp Ala Trp Val Leu Leu Thr Gly Glu Asn Gly Thr Gly Lys Glu Leu

 165 170 175

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180 185 190

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15 gca ggt cgt ttt gag ttg gca cat aaa gga aca tta ttt ctt gat gaa 720
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225 230 235 240

20 ata gga gat atg agt tta aaa aca caa gca aaa att ttg cgt att ttg 768
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245 250 255

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Gln Glu Gln Cys Phe Glu Lys Ile Gly Ser Val Arg Thr Ile Lys Val
260 265 270

25 gat gta aga gtt att gca gca aca aat aag aat ctt gaa gac gct att 864
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30 agc gat gga aca ttt cgt caa gat ttg tat tat cgc tta cga gtt gtt 912
Ser Asp Gly Thr Phe Arg Gln Asp Leu Tyr Tyr Arg Leu Arg Val Val
290 295 300

35 cca ttg cat ctt ccc cct ctt cgt gaa cgt gat tct gat att gag cta 960
Pro Leu His Leu Pro Pro Leu Arg Glu Arg Asp Ser Asp Ile Glu Leu
305 310 315 320

40 tta tta aat agg ttt gtg att cag ttg agt aaa cgt tat aga cgt gag 1008
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325 330 335

ccg cct att ttt tta gat gag gtc ttc cct gta ttg aaa caa tat tgt 1056
Pro Pro Ile Phe Leu Asp Glu Val Phe Pro Val Leu Lys Gln Tyr Cys
340 345 350

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 ctt ccc gat ata gat ttt aac cag gct aaa ata gct ttt gaa cca aaa 1248
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 15 ttt tta act gaa aaa tta cat gct tat caa gga aat att acc cga tta 1296
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 20 gca gaa gct att gga ctt gaa aga agt tat tta tat aga aag cta aaa 1344
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 35 40 45

 Leu Val Phe Leu Asp Ile Trp Leu Pro Gly Met Asp Gly Leu Met Ala
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 Leu Asp His Ile Gln Ala Leu His Gln Glu Leu Pro Val Ile Met Ile

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	Leu Leu Arg Thr Val Leu Pro Glu Glu Ser Glu Phe Ile Gly Gln Ser						
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15	Pro Val Ile Leu Lys Phe Lys Ser Leu Leu Ser Gln Val Ala Pro Thr						
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	Asp Ala Trp Val Leu Leu Thr Gly Glu Asn Gly Thr Gly Lys Glu Leu						
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	Ile Ala Val Asn Cys Ala Ala Ile Pro Glu Glu Leu Ile Glu Ser Glu						
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	Leu Phe Gly His Glu Lys Gly Ala Phe Thr Gly Ala Asp Ala Ser Arg						
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	Ser Asp Gly Thr Phe Arg Gln Asp Leu Tyr Tyr Arg Leu Arg Val Val						
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45	Pro Leu His Leu Pro Pro Leu Arg Glu Arg Asp Ser Asp Ile Glu Leu						
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							320

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Leu Pro Asp Ile Asp Phe Asn Gln Ala Lys Ile Ala Phe Glu Pro Lys
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20 Phe Leu Thr Glu Lys Leu His Ala Tyr Gln Gly Asn Ile Thr Arg Leu
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 Asn Leu Gln Val Asn Phe Ser Asn Pro Tyr His Gln Thr Asp Ile Glu
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5 ttt aat aaa cct gaa gtt ata gtt gct ata cgt aat ggt agt aca gtt 192
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 85 90 95

20 ata tta tta gct tca gca cca tta cca gcg att caa gct ata aac tca 336
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 100 105 110

aat ggc aac ctt att cgt tta gat aca ctc ccc att act cat caa tct 384
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45 Phe Asn Lys Pro Glu Val Ile Val Ala Ile Arg Asn Gly Ser Thr Val
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Ile Thr Pro Ala Lys Gln Leu Leu Pro Lys Ala Ser Phe Arg Leu Phe
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 Gly Tyr Leu Met Ala Lys Gly Asn Leu Ala Leu Leu Phe Gln Pro Ala
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 Glu Leu Val Ile Ile Ile Gly Ala Ala Leu Gly Ala Phe Phe Ala Ser
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40 cag acg aaa tat tca ttt act ctg gtc att aaa aat tta tca cac att 192
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	gta gaa tat gga aga cgt gcc ata cct aat aca ttt cgt cca tca ttt	816

- 16 -

Val Ala Ala Val Leu Gly Val Val Ile Thr Met Gly Lys Ile Asn Glu
180 185 190

5 Pro Pro Glu Val Leu Gly His Tyr Ile Gly Ala Ala Leu Val Gly Thr
195 200 205

Phe Ile Gly Ile Leu Phe Cys Tyr Gly Phe Phe Gly Pro Met Gly Ser
210 215 220

10 Lys Leu Glu Thr Ser Ala Glu Glu Ala His Phe Tyr Tyr Asn Ser Ile
225 230 235 240

Lys Glu Ala Val Ala Ala Ala Ile Arg Gly Ser Thr Pro Met Ile Ala
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Val Glu Tyr Gly Arg Arg Ala Ile Pro Asn Thr Phe Arg Pro Ser Phe
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20 Ser Glu Met Glu Glu Arg Leu Lys Thr Gly
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atg gct ttc ttt cta ctg atg tgg att ctt gca atg aca ccc cct gag 96
Met Ala Phe Phe Leu Leu Met Trp Ile Leu Ala Met Thr Pro Pro Glu
40 20 25 30

gtt aaa gaa ggt ctt gct gca tat ttt tct tca tct gat gct aca ttt 144
Val Lys Glu Gly Leu Ala Ala Tyr Phe Ser Ser Ser Asp Ala Thr Phe
35 40 45

45 aaa aca cct gat agt tcg cca atc tct aac aat cct ctt atc aac caa 192

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5	ata	gat	aaa	ctt	gat	act	cga	caa	tta	aaa	att	aat	gaa	aca	gaa	caa	240
	Ile	Asp	Lys	Leu	Asp	Thr	Arg	Gln	Leu	Lys	Ile	Asn	Glu	Thr	Glu	Gln	
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	Ser	His	Tyr	Ala	Leu	Ala	Asn	Lys	Leu	Lys	Lys	Met	Leu	Met	Ala	Asp	
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15	gct	atc	cca	cag	tca	gca	aca	gga	ata	agt	gct	gac	gat	gtt	ggg	gta	336
	Ala	Ile	Pro	Gln	Ser	Ala	Thr	Gly	Ile	Ser	Ala	Asp	Asp	Val	Gly	Val	
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	Leu	Leu	Arg	Val	Asn	Ser	Asn	Ser	Thr	Phe	Phe	Pro	Gly	Thr	Ala	Thr	
			115					120					125				
25	ctt	aca	ccc	gaa	ggg	aaa	aaa	gtt	atg	gga	act	gtt	tta	gcc	gtt	ctc	432
	Leu	Thr	Pro	Glu	Gly	Lys	Lys	Val	Met	Gly	Thr	Val	Leu	Ala	Val	Leu	
		130						135				140					
30	cgt	gaa	tat	aat	ctt	tac	ctt	gtg	ata	cgt	ggc	cat	gct	gat	att	ggg	480
	Arg	Glu	Tyr	Asn	Leu	Tyr	Leu	Val	Ile	Arg	Gly	His	Ala	Asp	Ile	Gly	
	145					150					155					160	
35	gaa	ata	aca	aaa	ggc	agc	cct	ttt	gct	tct	aac	tgg	gaa	ctt	tca	gga	528
	Glu	Ile	Thr	Lys	Gly	Ser	Pro	Phe	Ala	Ser	Asn	Trp	Glu	Leu	Ser	Gly	
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40	gct	cgt	gca	gct	gca	gct	gca	cag	tat	ctt	gta	gag	cac	ggg	ata	aag	576
	Ala	Arg	Ala	Ala	Ala	Ala	Ala	Gln	Tyr	Leu	Val	Glu	His	Gly	Ile	Lys	
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45	gct	tca	cga	att	cgc	tct	gta	gga	tat	gca	gat	aca	aga	cct	cta	gaa	624
	Ala	Ser	Arg	Ile	Arg	Ser	Val	Gly	Tyr	Ala	Asp	Thr	Arg	Pro	Leu	Glu	
			195					200					205				
50	cct	agt	tct	cct	gaa	gga	agt	aca	aaa	aat	cgt	cgt	ata	gaa	ttc	tat	672
	Pro	Ser	Ser	Pro	Glu	Gly	Ser	Thr	Lys	Asn	Arg	Arg	Ile	Glu	Phe	Tyr	
		210						215				220					
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15 Val Lys Glu Gly Leu Ala Ala Tyr Phe Ser Ser Ser Asp Ala Thr Phe
      35              40              45

Lys Thr Pro Asp Ser Ser Pro Ile Ser Asn Asn Pro Leu Ile Asn Gln
      50              55              60

20 Ile Asp Lys Leu Asp Thr Arg Gln Leu Lys Ile Asn Glu Thr Glu Gln
      65              70              75              80

Ser His Tyr Ala Leu Ala Asn Lys Leu Lys Lys Met Leu Met Ala Asp
25      85              90              95

Ala Ile Pro Gln Ser Ala Thr Gly Ile Ser Ala Asp Asp Val Gly Val
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30 Leu Leu Arg Val Asn Ser Asn Ser Thr Phe Phe Pro Gly Thr Ala Thr
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Leu Thr Pro Glu Gly Lys Lys Val Met Gly Thr Val Leu Ala Val Leu
      130             135             140

35 Arg Glu Tyr Asn Leu Tyr Leu Val Ile Arg Gly His Ala Asp Ile Gly
      145             150             155             160

Glu Ile Thr Lys Gly Ser Pro Phe Ala Ser Asn Trp Glu Leu Ser Gly
40      165             170             175

Ala Arg Ala Ala Ala Ala Ala Gln Tyr Leu Val Glu His Gly Ile Lys
      180             185             190

45 Ala Ser Arg Ile Arg Ser Val Gly Tyr Ala Asp Thr Arg Pro Leu Glu
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Pro Ser Ser Pro Glu Gly Ser Thr Lys Asn Arg Arg Ile Glu Phe Tyr
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5 Phe His Arg Pro Glu Val Met Ser Tyr Gly Val Val Tyr
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tta tgc tca atg atg gaa gct gct ata tac tct atc cct att act tat 96
 Leu Cys Ser Met Met Glu Ala Ala Ile Tyr Ser Ile Pro Ile Thr Tyr
 25 20 25 30

att gaa cac ctt cgt gaa cag gga agc aaa aaa gga gaa aaa ctt tat 144
 Ile Glu His Leu Arg Glu Gln Gly Ser Lys Lys Gly Glu Lys Leu Tyr
 35 40 45

30 tat tta cat agt aat att gat cag cct att aca gcc gta tta ata ttg 192
 Tyr Leu His Ser Asn Ile Asp Gln Pro Ile Thr Ala Val Leu Ile Leu
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35 aat act ata gca aat act gct gga gct gcc ctt gct gga gca att gct 240
 Asn Thr Ile Ala Asn Thr Ala Gly Ala Ala Leu Ala Gly Ala Ile Ala
 65 70 75 80

aca aca aca ctt cat gaa tct act aag cct ttc ttt gca gca atc ctc 288
 40 Thr Thr Thr Leu His Glu Ser Thr Lys Pro Phe Phe Ala Ala Ile Leu
 85 90 95

acc ttg ctt att tta gct ttt ggg gaa att ata cct aaa aca cta ggt 336
 Thr Leu Leu Ile Leu Ala Phe Gly Glu Ile Ile Pro Lys Thr Leu Gly
 45 100 105 110

F0040360.F0004

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gtt gct tac tct aaa cgt att gct ata att ctc ctt aat cct ctc tct 384
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 115 120 125

5 att ctt ata gtt act tta aaa ccc ctt att atg ctt tca agc tac tta 432
 Ile Leu Ile Val Thr Leu Lys Pro Leu Ile Met Leu Ser Ser Tyr Leu
 130 135 140

10 aca cga ctt gtt tca cct cga aaa cgt cct aca gtt aca gaa gat gac 480
 Thr Arg Leu Val Ser Pro Arg Lys Arg Pro Thr Val Thr Glu Asp Asp
 145 150 155 160

15 atc cgt gca ctt aca agt ctt tcc aga gag tct ggt cgt att aag cca 528
 Ile Arg Ala Leu Thr Ser Leu Ser Arg Glu Ser Gly Arg Ile Lys Pro
 165 170 175

20 tat gaa gaa cat gtc ata aaa aat atc ctt agt ctt gat tta aaa tat 576
 Tyr Glu Glu His Val Ile Lys Asn Ile Leu Ser Leu Asp Leu Lys Tyr
 180 185 190

gct cat gaa att atg act ccc aga act atg gtc ttt tca ctt cat gaa 624
 Ala His Glu Ile Met Thr Pro Arg Thr Met Val Phe Ser Leu His Glu
 195 200 205

25 aac ctt act gtc tct gaa gct tat agc aac ccc aaa ata tgg aac tat 672
 Asn Leu Thr Val Ser Glu Ala Tyr Ser Asn Pro Lys Ile Trp Asn Tyr
 210 215 220

30 agt cgc atc cct act tat gga gaa aat aac gaa gac att act ggc att 720
 Ser Arg Ile Pro Thr Tyr Gly Glu Asn Asn Glu Asp Ile Thr Gly Ile
 225 230 235 240

35 atc caa cga tat gaa att gga cga tat atg acc aat gga gaa aca gaa 768
 Ile Gln Arg Tyr Glu Ile Gly Arg Tyr Met Thr Asn Gly Glu Thr Glu
 245 250 255

40 aaa aaa ctt tta gaa att atg caa cca gca aaa ttt gtc ctt gaa agt 816
 Lys Lys Leu Leu Glu Ile Met Gln Pro Ala Lys Phe Val Leu Glu Ser
 260 265 270

caa act gta gat cat tta ctt ctt gca ttt tta gaa gaa aga caa cat 864
 Gln Thr Val Asp His Leu Leu Leu Ala Phe Leu Glu Glu Arg Gln His
 275 280 285

45 ctt ttt att gta ctt gat gag tat ggg gga tta tct ggt gtt gtt tcc 912
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T00433150-10004

- 21 -

290 295 300

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 5 305 310 315 320

agt gat aca aca cct gat ctt aga gca ctt gca aaa aaa aga cat agt 1008
 Ser Asp Thr Thr Pro Asp Leu Arg Ala Leu Ala Lys Lys Arg His Ser
 325 330 335

10 gca tta atc caa aat aat aaa aat act ctt tta aaa taa 1047
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30 Tyr Leu His Ser Asn Ile Asp Gln Pro Ile Thr Ala Val Leu Ile Leu
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Asn Thr Ile Ala Asn Thr Ala Gly Ala Ala Leu Ala Gly Ala Ile Ala
 35 65 70 75 80

Thr Thr Thr Leu His Glu Ser Thr Lys Pro Phe Phe Ala Ala Ile Leu
 85 90 95

40 Thr Leu Leu Ile Leu Ala Phe Gly Glu Ile Ile Pro Lys Thr Leu Gly
 100 105 110

Val Ala Tyr Ser Lys Arg Ile Ala Ile Ile Leu Leu Asn Pro Leu Ser
 115 120 125

45 Ile Leu Ile Val Thr Leu Lys Pro Leu Ile Met Leu Ser Ser Tyr Leu

10030160-110901

- 22 -

130 135 140

Thr Arg Leu Val Ser Pro Arg Lys Arg Pro Thr Val Thr Glu Asp Asp
 145 150 155 160

5
 Ile Arg Ala Leu Thr Ser Leu Ser Arg Glu Ser Gly Arg Ile Lys Pro
 165 170 175

10
 Tyr Glu Glu His Val Ile Lys Asn Ile Leu Ser Leu Asp Leu Lys Tyr
 180 185 190

Ala His Glu Ile Met Thr Pro Arg Thr Met Val Phe Ser Leu His Glu
 195 200 205

15
 Asn Leu Thr Val Ser Glu Ala Tyr Ser Asn Pro Lys Ile Trp Asn Tyr
 210 215 220

20
 Ser Arg Ile Pro Thr Tyr Gly Glu Asn Asn Glu Asp Ile Thr Gly Ile
 225 230 235 240

Ile Gln Arg Tyr Glu Ile Gly Arg Tyr Met Thr Asn Gly Glu Thr Glu
 245 250 255

25
 Lys Lys Leu Leu Glu Ile Met Gln Pro Ala Lys Phe Val Leu Glu Ser
 260 265 270

Gln Thr Val Asp His Leu Leu Leu Ala Phe Leu Glu Glu Arg Gln His
 275 280 285

30
 Leu Phe Ile Val Leu Asp Glu Tyr Gly Gly Leu Ser Gly Val Val Ser
 290 295 300

35
 Leu Glu Asp Val Leu Glu Thr Met Leu Gly Arg Glu Ile Val Asp Glu
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Ser Asp Thr Thr Pro Asp Leu Arg Ala Leu Ala Lys Lys Arg His Ser
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 340 345

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 165 170 175

5 cca tta gcc aaa ata aaa aaa act caa tac ata att aat cgg atg gat 576
 Pro Leu Ala Lys Ile Lys Lys Thr Gln Tyr Ile Ile Asn Arg Met Asp
 180 185 190

10 tat aca ttt gat att gat tta gta ata aga caa gga ccg tta ctc cat 624
 Tyr Thr Phe Asp Ile Asp Leu Val Ile Arg Gln Gly Pro Leu Leu His
 195 200 205

15 atg ggt aaa gta caa cct caa cat aat ctc aat att tca aca ata ttc 672
 Met Gly Lys Val Gln Pro Gln His Asn Leu Asn Ile Ser Thr Ile Phe
 210 215 220

20 cta aat aaa att gct aca tgg aag gaa gga agg gta tgg aac aat gca 720
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 225 230 235 240

ctc ctt gat tct tat cga aca cgg ctt caa caa aca ggc ctt ttc agt 768
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 245 250 255

25 tct ata act ctc aat cca agg aat caa aaa gaa caa aat ggt aac acc 816
 Ser Ile Thr Leu Asn Pro Arg Asn Gln Lys Glu Gln Asn Gly Asn Thr
 260 265 270

30 tct ata gaa ctt gtt gca aca gaa gcc cct cca agg act att agt ggt 864
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 275 280 285

35 ggc tta caa tac tct tct gat caa ggt att ggt gca cgt ggg act tgg 912
 Gly Leu Gln Tyr Ser Ser Asp Gln Gly Ile Gly Ala Arg Gly Thr Trp
 290 295 300

40 gaa cat cga aat gtt ttt ggt aat gga gaa ctt ttt cgt ata aca gca 960
 Glu His Arg Asn Val Phe Gly Asn Gly Glu Leu Phe Arg Ile Thr Ala
 305 310 315 320

cca ata agt cga gat gat caa aaa att atg gca aac ttc caa aaa cca 1008
 Pro Ile Ser Arg Asp Asp Gln Lys Ile Met Ala Asn Phe Gln Lys Pro
 325 330 335

45 gcc ttt ggc cgt cca aat caa tca tta att agt gaa gca caa ctt aaa 1056
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10010150 - 110904

- 25 -

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5 tat tta cga aaa aaa aat ttc ctg act tta aaa aaa tca ata tat tgg 1680
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10 ggg gta ggc ctg ggg cta cga tat tat aca agt ttt gcc ccc ata cgt 1728
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 565 570 575

15 tta gat ata gca act cca ctt caa gat aga agc cat aat aaa cac ttt 1776
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20 caa ctt tat att agt att ggg caa gca ttc taa tga 1812
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 35 40 45

Pro Asn Leu Ala Thr Glu Met Glu Thr His Ser Glu Leu Val Lys Leu
 50 55 60

40 Ala Asn Gln Ser Leu Asp Ser Lys Ile Gly Leu Asn Leu Arg Val Lys
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Glu Asp Ile Ser Thr Ala Gln Lys Ile Leu Asp Ser Asn Gly Tyr Tyr
 85 90 95

45 Ser Gly Ser Val Glu Gly Lys Ile Asp Trp Gln Thr Asn Pro Ile Ser

10010160-100001

- 27 -

100 105 110

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130 135 140

10 Glu Glu Phe Asn Leu Ser Lys Gly Asn Pro Ala Leu Ala Val Asn Ile
145 150 155 160

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165 170 175

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180 185 190

Tyr Thr Phe Asp Ile Asp Leu Val Ile Arg Gln Gly Pro Leu Leu His
195 200 205

20 Met Gly Lys Val Gln Pro Gln His Asn Leu Asn Ile Ser Thr Ile Phe
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25 Leu Asn Lys Ile Ala Thr Trp Lys Glu Gly Arg Val Trp Asn Asn Ala
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245 250 255

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260 265 270

Ser Ile Glu Leu Val Ala Thr Glu Ala Pro Pro Arg Thr Ile Ser Gly
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305 310 315 320

40 Pro Ile Ser Arg Asp Asp Gln Lys Ile Met Ala Asn Phe Gln Lys Pro
325 330 335

45 Ala Phe Gly Arg Pro Asn Gln Ser Leu Ile Ser Glu Ala Gln Leu Lys
340 345 350

10030350 - 1109004

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20	Phe	Asp	Phe	Ser	Phe	Tyr	Ile	Asp	Val	Leu	Lys	Thr	Gly	Lys	Leu	Ile
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30	500				505				510							
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	545				550				555				560			
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	Leu	Asp	Ile	Ala	Thr	Pro	Leu	Gln	Asp	Arg	Ser	His	Asn	Lys	His	Phe
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gca ttt acg tta ttt tta gga ctt att att aca ggc att ctt ttt ata 96
Ala Phe Thr Leu Phe Leu Gly Leu Ile Ile Thr Gly Ile Leu Phe Ile
20 20 25 30

cgg acc tct aca ggc att gct tgg att aaa aat aca gtt tct tct tta 144
 Arg Thr Ser Thr Gly Ile Ala Trp Ile Lys Asn Thr Val Ser Ser Leu
 35 40 45

25 ctt caa caa caa gga att ata cta caa gta tct tca att att gga cca 192
Leu Gln Gln Gln Gly Ile Ile Leu Gln Val Ser Ser Ile Ile Gly Pro
 50 55 60

30 ttc cca gaa caa att act att aat gaa ctt agc ctt agt gat gtg aat 240
Phe Pro Glu Gln Ile Thr Ile Asn Glu Leu Ser Leu Ser Asp Val Asn
65 70 75 80

35 gga act tac ctt aca ata tct aac tta gaa atc caa tca aac tta tgg 288
Gly Thr Tyr Leu Thr Ile Ser Asn Leu Glu Ile Gln Ser Asn Leu Trp
85 90 95

gct tta ttc aaa ggt caa ctt gaa att ctg tct ttt gaa ctt aat gat 336
Ala Leu Phe Lys Gly Gln Leu Glu Ile Leu Ser Phe Glu Leu Asn Asp
40 100 105 110

ctt gta tta tat cgc tta ccc tca aat aat aat cta aaa aaa tca tct 384
Leu Val Leu Tyr Arg Leu Pro Ser Asn Asn Asn Leu Lys Lys Ser Ser
115 120 125

45 aca agt ttt gtg tta cct cac ata tca ttt gat tta act cca tgg tgg 432

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	Thr Glu His Ile Arg Ile Gln Asn Ile His Ile Asn Asn Thr Gln Leu	
	145 150 155 160	
10	tcc tct gat att ata ggt att cca ttg gta tta tcc ctt gag ggt gat	528
	Ser Ser Asp Ile Ile Gly Ile Pro Leu Val Leu Ser Leu Glu Gly Asp	
	165 170 175	
15	ggg aca tta aca aat tgg aat gga aca ttt caa cta tcc tct tct aac	576
	Gly Thr Leu Thr Asn Trp Asn Gly Thr Phe Gln Leu Ser Ser Ser Asn	
	180 185 190	
	aaa aca aaa att ata gga acg ctt cgt tac caa ggg aat aag aca caa	624
	Lys Thr Lys Ile Ile Gly Thr Leu Arg Tyr Gln Gly Asn Lys Thr Gln	
	195 200 205	
20	ttt ttt gaa tat gtt cat cct aca cgg ata gta aca cta gag ata gac	672
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	210 215 220	
25	agc gta gct gat aaa aag tca tat aat aat agt atc ctt gaa caa cct	720
	Ser Val Ala Asp Lys Lys Ser Tyr Asn Asn Ser Ile Leu Glu Gln Pro	
	225 230 235 240	
30	cta cat tta cac ctt tct att tat cct gaa cat aat aga att atc tta	768
	Leu His Leu His Leu Ser Ile Tyr Pro Glu His Asn Arg Ile Ile Leu	
	245 250 255	
35	cac tca tta cta gct gaa tat ggt agc tgg tta ctt aca tca gaa agt	816
	His Ser Leu Leu Ala Glu Tyr Gly Ser Trp Leu Leu Thr Ser Glu Ser	
	260 265 270	
	att gaa gta tct aat gag caa tta aaa gga aat att tta tta aaa tat	864
	Ile Glu Val Ser Asn Glu Gln Leu Lys Gly Asn Ile Leu Leu Lys Tyr	
	275 280 285	
40	aat gga gaa gct act cat caa ctt cct ata aaa aaa ctt aac tca tca	912
	Asn Gly Glu Ala Thr His Gln Leu Pro Ile Lys Lys Leu Asn Ser Ser	
	290 295 300	
45	att acc ctc agt ggc tca cta aat aaa cct aat ttt agt ata caa atg	960
	Ile Thr Leu Ser Gly Ser Leu Asn Lys Pro Asn Phe Ser Ile Gln Met	
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5 aca tta cct gaa att aac att aca aaa aac ata ata gat ctt caa aca 1008
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10 gaa ctt gtt att aat cta gga ctt ttc tct act cac tct gat att ctt 1056
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20 acc tta gag cat gca acc tta aca tct cca gaa atg cat ttt tcc cta 1200
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25 tct gga gaa ttt aat agt ctt cta gga aat atc gat gca aac cta aaa 1248
 Ser Gly Glu Phe Asn Ser Leu Leu Gly Asn Ile Asp Ala Asn Leu Lys
 405 410 415

30 ggt aat act cca act ctt agt ata ttt tct tct ctt ctt gga cta cct 1296
 Gly Asn Thr Pro Thr Leu Ser Ile Phe Ser Ser Leu Leu Gly Leu Pro
 420 425 430

35 gat ctt act ggg caa agt aac att act ata gga tta cac cgt caa ggg 1344
 Asp Leu Thr Gly Gln Ser Asn Ile Thr Ile Gly Leu His Arg Gln Gly
 435 440 445

40 tct tcc tct tca ata gaa gga aca gca act gtc tca ctt aat aat atg 1392
 Ser Ser Ser Ser Ile Glu Gly Thr Ala Thr Val Ser Leu Asn Asn Met
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45 aac tgg gga gta caa gca tta cag ggg aca tta ggt gat aat gca act 1440
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 465 470 475 480

45 cta agt gga ata tat aat tta act ccc ata gac tgg tct att tct tta 1488
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 485 490 495

45 aac aaa ttg aaa tta aca gca aag aat gtt tat gct gaa ggc ctt att 1536

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5 aat ttt caa aaa aaa tac ata gat agc tct ata aat ctt ata att cct 1584
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10 aac ctt cag cta ata gct cct cct ata tct gga gag tta caa tcc tta 1632
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15 att aca gtg tct gga aaa ctt gac gca cct tct ata gaa agc aaa att 1680
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30 agt aat tgg gga atc cta cct acg gaa ata cta gta gaa aaa att ata 1872
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35 gga aat ata tta gga gta aat ctt gat ggt aat att aaa ata aca aaa 1920
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	Asn Ala Asn Ala Ile Ile Lys Glu Val Ser Leu Leu Ser Phe Gln Pro	
40	835 840 845	
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	Phe Ser Ile Leu Leu Pro Gln Gly Asn Ile Asn Gly His Ile Thr Leu	
	850 855 860	
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	aca gga ata cct agt aaa cct aaa gga aca ctc tca ttt gat att cta	2640

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5 aac ata cat tat cca agg cca aat cca tca ata gca aac tta cat gta 2688
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10 gaa ggg gaa att ata tct tct cct aac aat ata tgt aaa ctt aat gca 2736
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15 acc cta aca gaa aaa aaa gag cct ata cct ata tca ata caa gca aca 2784
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25 agg cct ttt tct gcc cat atc aag tgg act gga ata tta gat aca ctt 2880
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30 tgg aaa ctc att cca ctt act gat tac att atg gct ggg aat gga tct 2928
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45 tac tta gaa aat atc aat gct aaa tta cag gtc ttt tct aat aga atc 3072
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45 tcc cat att caa gct aca gca tct gat ggt aaa caa ggt agt ata caa 3120
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45 ctt att ggt aat att ggc tca tct aaa gaa cac ttt cct ttg tct att 3168
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- 35 -

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Asn Pro Asn Ile Thr Phe Ser Ser Thr Pro Pro Leu Pro Gln Asp Glu
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10 ata caa gcc ata caa ctt gct caa gaa tta gca aac tta aca gga ttt 3840
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20 tta gat ata ctt agc tta ggg aca act tct aat aga aaa gcc aat aca 3936
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25 tcc aac tca aac gat caa ata gaa gat atc cct gtt ata gaa cta ggt 3984
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30 aaa tat att aca gac act gtt tat gtt ggt gtt gaa caa agt tat tta 4032
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35 gat agt aat gat act ggg gca aga ata tca gtt gaa ctt gca cct aat 4080
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40 ttt aat ctt gaa ggt aga aca ggg act caa tat agt gag ata ggt att 4128
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45	Leu	His	Leu	His	Leu	Ser	Ile	Tyr	Pro	Glu	His	Asn	Arg	Ile	Ile	Leu

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Asn Lys Leu Lys Leu Thr Ala Lys Asn Val Tyr Ala Glu Gly Leu Ile
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5 Asn Phe Gln Lys Lys Tyr Ile Asp Ser Ser Ile Asn Leu Ile Ile Pro
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Asn Leu Gln Leu Ile Ala Pro Pro Ile Ser Gly Glu Leu Gln Ser Leu
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10 Ile Thr Val Ser Gly Lys Leu Asp Ala Pro Ser Ile Glu Ser Lys Ile
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Phe Ser Ser Gln Leu Thr Trp Asn Ala Leu Gln Leu Asn Asn Pro Gln
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Leu Ile Ile Thr Thr Thr Gln Ser Ser Ser Ser Ala Ile Lys Gly Asn
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20 Ile Thr Leu Ser Ala Glu Pro Ala Ser Ser Glu Ala Leu Thr Phe Ser
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Ser Asn Trp Gly Ile Leu Pro Thr Glu Ile Leu Val Glu Lys Ile Ile
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Lys Asp Ile Ala Asn Ile Leu Gln Ile Pro Ile Arg Gly Ser Ala Ser
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Val Ser Pro Gln Gln Phe Val Leu Asn Asn Cys Ser Leu Ala Ile Leu
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Trp Lys Leu Ile Pro Leu Thr Asp Tyr Ile Met Ala Gly Asn Gly Ser
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Leu Asp Ala Ser Leu Ser Gly Thr Leu Asp Ser Pro Thr Tyr Ala Ile

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40	ctattgatgg atttgcctt gg	22
	<210> 34	
	<211> 20	<212>
	DNA	
45	<213> Artificial Sequence	

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<220>

<223> Description of Artificial Sequence:
Oligonucleotide probe/primer

5 <400> 34

gtgctggtac atatgaagac

20

<210> 35

10 <211> 20

<212> DNA

<213> Artificial Sequence

<220>

15 <223> Description of Artificial Sequence:
Oligonucleotide probe/primer

<400> 35

ttcatcacct tctattacag

20

20

<210> 36

<211> 20

<212> DNA

25 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Oligonucleotide probe/primer

30

<400> 36

ggaaactatt tcatcttgag

20

35 <210> 37

<211> 20

<212> DNA

<213> Artificial Sequence

40 <220>

<223> Description of Artificial Sequence:
Oligonucleotide probe/primer

<400> 37

45 attaggtgca agttcaactg

20

T0030150-100001

- 48 -

<210> 38
 <211> 20
 <212> DNA
 5 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:
 Oligonucleotide probe/primer
 10
 <400> 38
 ttagatagt aatgatactg 20

 15 <210> 39
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 <212> DNA
 <213> Artificial Sequence

 20 <220>
 <223> Description of Artificial Sequence:
 Oligonucleotide probe/primer

 <400> 39
 25 ttattatatt atgttttttg taatgttaat ttcagg 36

 <210> 40
 <211> 28
 30 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:
 35 Oligonucleotide probe/primer

 <400> 40
 gacatatgaa taacacaaaa atactttc 28

 40
 <210> 41
 <211> 41
 <212> DNA
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 45 <220>

10030360-110904

<223> Description of Artificial Sequence:
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5 gaggatcctc tagagttaat caaactgtat ttttattgat g 41

<211> 31

<213> Artificial Sequence

<223> Description of Artificial Sequence:
Oligonucleotide probe/primer

gacatatgcg gacctctaca ggcattgctt g 31

<211> 24

<213> Artificial Sequence

<223> Description of Artificial Sequence:
Oligonucleotide probe/primer

gatcaggtag tccaagaaga gaag 24

35 <211> 45

<213> Artificial Sequence

40 <223> Description of Artificial Sequence:
Oligonucleotide probe/primer

ttggaggatc ctctagagtt atcaggttgt aattggtcca gatgg 45

45

5

10

15

20

25

30

35

40

45

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<400> 48
gaggatcctc tagagttaga atgcttgccc aatact 36
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[illegible]

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<210> 49
 <211> 39
 <212> DNA
 5 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: oligo

 10 <400> 49
 ttggaggatc ctctagagtt agaatgcttg cccaatact 39

 <210> 50
 <211> 32
 15 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: oligo
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 <400> 50
 ttgaccatgg ctacatcaat taccacttcc ac 32

 <210> 51
 25 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 30 <223> Description of Artificial Sequence: oligo

 <400> 51
 ggacatatga ataacacaaa aataactttc 29

 35 <210> 52
 <211> 44
 <212> DNA
 <213> Artificial Sequence

 40 <220>
 <223> Description of Artificial Sequence: oligo

 <400> 52
 ttggaggatc ctctagagtt aatcaaactg tatttttatt gatg 44
 45
 <210> 53

10010160-110001
 10010160-110001

- 52 -

<211> 32

<212> DNA

<213> Artificial Sequence

5 <220>

<223> Description of Artificial Sequence: oligo

<400> 53

ggacatatgc ggacctctac aggcattgct tg

32

10

<210> 54

<211> 20

<212> DNA

<213> Artificial Sequence

15

<220>

<223> Description of Artificial Sequence: oligo

<400> 54

tgaggattat taagttggag

20

20

<210> 55

<211> 20

25 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: oligo

<400> 55

gcatgcaacc ttaacatctc

20

30

<210> 56

35 <211> 20

<212> DNA

<213> Artificial Sequence

<220>

40 <223> Description of Artificial Sequence: oligo

<400> 56

tttctgatgt aagtaaccag

20

45

<210> 57

<211> 20

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<212> DNA

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<400> 57

20

<211> 20

<212> DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence: oligo

<400> 58

qgaacatttc aactatcctc

20

<210> 59

<211> 28

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Description of Artificial Sequence: oligo

<400> 59

gtaaggtaag ttccattcac

20

<210> 60

<211> 25

<212> DNA

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Description of Artificial Sequence: oligo

<400> 60

caacgtggat ccgaattcaa gcttc

25

<210> 61

<211> 17

<212> PRT

<213> Artificial Sequence

- 54 -

<220>

<223> Description of Artificial Sequence: Peptide

5 <400> 61

Met Gly Ser Gly Ser Gly Asp Asp Asp Asp Lys Leu Ala Leu Leu Thr
 1 5 10 15

Met

10

<210> 62

<211> 7

15 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peptide

20

<400> 62

Ala Thr Ser Ile Thr Thr Ser
 1 5

25

<210> 63

<211> 45

<212> PRT

<213> Artificial Sequence

30

<220>

<223> Description of Artificial Sequence: Peptide

<400> 63

35 Met His His His His His His Ser Ser Gly Leu Val Pro Arg Gly Ser
 1 5 10 15

Gly Met Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln His Met Asp
 20 25 30

40

Ser Pro Asp Leu Gly Thr Asp Asp Asp Asp Lys Ala Met
 35 40 45

45 <210> 64

<211> 50

40010150-4100001

<212> PRT

 $\langle 220 \rangle$

<400> 64

10

15

20

<210> 65

<211> 7

<212> PRT

<213> Artificial Sequence

 $\langle 220 \rangle$

<223> Description of Artificial Sequence: Peptide

<400> 65

30 Glu Phe Asn Leu Ser Lys Gly
 1 5

<210> 66

35 <211> 17

<212> PRT

<213> Artificial Sequence

<220>

40 <223> Description of Artificial Sequence: Peptide

<400> 66

Met Gly Ser Gly Ser Gly Asp Asp Asp Asp Lys Leu Ala Leu Gly His
1 5 10 15

45

Met

- 56 -

5 <210> 67
<211> 7
<212> PRT
<213> Artificial Sequence

10 <220>
<223> Description of Artificial Sequence: Peptide

15 <400> 67
Arg Thr Ser Thr Gly Ile Ala
1 5

20 <210> 68
<211> 21
<212> PRT
<213> Artificial Sequence

25 <220>
<223> Description of Artificial Sequence: Peptide

<400> 68
Asp Pro Asn Ser Ser Ser Val Asp Lys Leu Ala Ala Ala Leu Glu His
1 5 10 15

30 His His His His His
20